Scores:		Similarity matrix Threshold level of sim. Translation Frame M'-vatch penalty venalty G. size penalty Cutoff score Randomization group
Mean 52	SEARC	PAM-150 16% 6 1 5.00 0.05
Median 16	SEARCH STATISTICS	K-tuple Joining penalty Window size
Standard Deviation 89.65	0,1	nalty
viation		1 20 297

Number of residues: Number of sequences searched: Number of scores above cutoff:	Times:	Scores:
searched: ove cutoff:	CPU 00:00:00.00	Mean 52
1857 6 6		Median 16
	Total Elapsed 00:00:00:00.00	Standard Deviation 89.65

The scores below are sorted by initial score. Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

YNREARNAPDQSIXNGESILWWDGIG: 20 30 40 0 90 100 0 90 100 NAYCGDCLPRFYRKTRIGGLQDQBCI	Initial Score = 22 Optimized Score = 128 Significance = -0.33 Residue Identity = 7% Matches = 23 Mismatches = 258 Gaps = 0 Conservative Substitutions = 16 Translation Frame= 4  I	2. US-09-695-369A-27 (1-297) US-09-840-795-18 Sequence 18, Application US/09840795	270 280 290 X TGAETLGGNTVESTGDRLELNVPFEVPSP IWSISCFPVVWGARFHIHGTTRHV 290 300 310	200 210 220 230 240 250 ETSAESQVSENIFQTQPLNPILEDDCSSTSGFPTQESFTMASCTSESHSHWPHSPIECTELDLQKFSSSASY	130 140 150 150 170 180 190  VEADAPTVPPQEATLVALVSSLLVVETLAFLGLEFLYCKOFFNRHCQRGGLLOFEADKTAKEESLEPVPPSK	60 70 80 90 100 120 120 120 120 110 120 120 110 120 12	Sig 27 x 10 20 30 40 50 40 50 40 40 40 40 40 40 40 40 40 40 40 40 40	Initial Score = 235 Optimized Score = 237 Significance = 2.04 Residue Identity = 72% Matches = 213 Mismatches = 71 Gaps = 8 Conservative Substitutions = 1 Translation Frame= 3 \$\pi\$	1. US-09-695-369A-27 (1-297) US-09-840-795-18 Sequence 18, Application US/09840795	**** 2 standard deviations above mean **** US-09-840-795-18 Sequence 18, Application 10 235 237 2.04  **** 0 standard deviation from mean **** US-09-840-795-18 Sequence 18, Application 309 22 128 -0.33 US-09-840-795-18 Sequence 18, Application 309 17 123 -0.39 US-09-840-795-18 Sequence 18, Application 310 15 124 -0.41 US-09-840-795-18 Sequence 18, Application 309 13 112 -0.44 US-09-840-795-18 Sequence 18, Application 310 11 117 -0.46	Name Description Length Score Score Sig. Fr	וות דובר כו הפבר פרסופט דם:
										и франос	аше	

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4. US-09-695-369A-27 (1-297)
US-09-840-795-18 Sequence 18, Application US/09840795
                                                                                                                                                                                            Initial Score = Residue Identity =
                                                                                                                                                        Translation Frame=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Translation Frame=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Initial Score = Residue Identity =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -09-695-369A-27 (1-297)
uS-09-840-795-18 Sequence 18, Application US/09840795
                                                                                                                                                                                                                                                                                                                                                                               PVTDEXMALAPKWDSGTNPPQ
290 300 x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGNGRVDGSCSQMGLRYKSTS
290 300 X
RAEVDLYRSPIWEQEPSTRPLPAFPPWIAKKMSTGTNGDGVSPANGVVI.DRSVPRIVVMERVEMPTAQPALL {\bf x} 10 20 30 40 50 60 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  210 220 230 240 250 260 270 280 FQTQPLNPILEDDCSSTSGFPTQESFTMASCTSESHSHWPHSPIECTELDLQKFSSSASYTGAETLGGNTVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 280 290
YTGAETLGGNTVESTGDRLELNVPFEVPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLMTAQVMQLXHLWWPQLLLYLRGGQAVQXASPPSPXPQSLDSSCPGPHRWQVTHRPHWSQYSFSWQSMYGR 220 230 240 250 260 270 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WARLPGAQETWDSALVSLLGGTGKRDSSFAVLSASNCSKPPRWQCLLKNCLQXRKKSPRKARVNTTSRLLTS 80 90 100 110 120 130 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       290 X
STGDRLELNVPFEVPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATSVASXGGTVGASASTKLNWKAHXTSEVGVCFVHGMHSWSCRPPMRVFRXNIGKQSPQTALEVAVQLTFXT
150 160 170 180 190 200 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HHKCQSCITCAVINRVQKVNCTATSNAVCGDCLPRFYRKTRIGGLQDQECIPCTKQTPTSEVQCAFQLSLVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIDDSTGDATLTFVVAPAAFVPARRAGCAVGISTLSITTILGXLLSRTTPLAGDTPSPLVPVLIFLAIHGGK 220 230 240 250 260 270 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNKCGLLRGHCGCICLHXAQLEGTLNLRGGGLLRARDALLVLQASNACLSVEPGQTVPTDSIRGSCAVDLLN 150 160 200 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 150 160 170 180 190 200 ATLVALVSSLLVVFTLAFLGLEFFLYCKOFFNRHCORGGLLOFBADKTAKEESLFPVPPSKETSAESQVSENI
                                                                     MDCQENEYWDQWGRCVTCQRCGPGQELSKDCG-YGEGGDAYCTACPPRRYKSSWGHHKCQSCITCAVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \verb"MDCQENEYWDQWGRCVTCQRCGPG-----QELSKDCGYGEGGDAYCTACPPRRYKSSWG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10% Matches = 32
8 Conservative Substitutions
5
                                                                                                                                                                                                    10%
                                                                                                                                                                                                    15 Optimized Score = 10% Matches =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 Optimized Score =
                                                                                                                                                                             Conservative Substitutions
                                                                                                                                                                                               124 Significance = -0.41
31 Mismatches = 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 Significance = -0.39
32 Mismatches = 241
```

Translation Frame-Initial Score = Residue Identity =

10

20

30

40

50

60

6. US-09-695-369A-27 (1-297) US-09-840-795-18 Sequence 18, Application US/09840795

11 Optimized Score = 7% Matches = 12 Conservative Substit

117 Significance = -0.46
24 Mismatches = 261
utions = 12

Conservative Substitutions

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5. US-09-695-369A-27 (1-297)
US-09-840-795-18 Sequence 18, Application US/09840795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Translation Frame=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Residue Identity =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Initial Score
HTVPIGPSTHFLGNPWWEGRXRTSRWLLLPNG 270 280 290 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QQRRNLSSPCHPARRPVLSPKSLGPLAALPSCSLWTLFLYHNSSRGLKCDVHTSXXPTDGAYPIPSHQRIDS
210 220 230 240 250 260 270 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 90 100 110 120 130 140 VNCTATSNAVCGDCLPRYKKTRIGG--LQDQECIPCTKQTFTSEVQCAFQLSLVEADAPTVPPQEATLVAL
                                                                                              LELNVPFEVPSP
                                                                                                                                                                                                                                                                                    220 230 240 250 260 270 280 LIPTLEDDCSSTSGFFTQESFTMASCTSESHSHWYHSPIECTELDLQKFSSSASYTGAETLGGNTVESTGDR
                                                                                                                                                                                                                                                                                                                                                                                          GRRAPGRPGXTPLAGCSPVQQVWPPEGALWVHLPPLSSTGRHIEPQRWGSASCTGCTLGPAGLQCVSFGRTW
130 140 150 160 170 180 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFQAPAAVVYXEQSPERTTGQGCQGPKRIGTQHWSPCWVARGREIPPILFYQPQTAANLHAGNVCXRTACSR 60 70 80 100 110 120
                                                                                                                                                                                         ANSPHRQHXRXLCSXPSEHDXXQHRXCNSDICGGPSCFCTCEEGRLCSRHLHPLHNHNPWIAPVQDHTVGRX 200 210 250 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 20 30 40 50 50 60 70 MDCQENEYWDQWGRCVTCQRCGPGQELSKDCGYGEGGDAYCTACPPRRYKSSWGHHKCQSCITCAVINRVQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFHKDXSGAFLASLLXSGEPDSTFMGLPDM
290 x 300 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 230 240 250 260 270 280 PINPILEDDCSSISGFFTQESFTMASCISESHSHWVHSFIECTELDLQKFSSSASYTGAETLGGNTVESTGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPPLIRFNVPSSXAXWRQMHPQCPLRRPHLLHWXAACXWCLPWPSWGSSSSTASSSSTDIASVEVCCSLRLIK 140 150 160 170 180 190 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTKAAGATTNVRVASPVLSSIVFRRSTAQLPLMLSVGTVCPGSTE------RHALEACRTKSASRÅRSR
80 90 100 110 120 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70 80 100 110 120 130 140 RVQKVNCTATSNAVCGDCLPREYRKTRIGGLQDQECIPCTKQTPTSEVQCAFQLSLVEADAPTVPPQEATLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {\tt VSSLLVVFTLAFLGLEFLYCKQFFNRHCQRGGLLQFEADKTAKEESLFPVPPSKETSAESQVSENI-FQTQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RLELNVPFEVPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALVSSILVVFTLAFIGLFFLYCKQFFNRHCQRGGLLQFEADKTAKEESLFPVPPSKETSAESQVSENIFQTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HVWXSHECGIWLPRLQQGSKKCSRSVLVKWRINPLVGWDRICPICRVLALVDI X 10 20 30 40 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 Optimized Score = 9% Matches =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative Substitutions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
```